

Thu Mar 24 08:02:13 2005

us-10-6

Db	234	QIHVSFDCNVNQASNLMTAPENSPNTDGIHVTGTQNIHIISSCVIGTGGDDCISVNGSR	293
Qy	281	NVQATNITCGPCHGISISGLSGNSEAVSVNVTNEAKIIIGAENGVRITKWGGSGOASN	340
Db	294	KVRVNDITCGPCHGISISGLSGNSEAHVSDVVVNGAKLCGTTNGVRITKWGGSGOASN	353
Qy	341	IKFLNVMQDVKYPIIIDQNYCDRVEPCIQQFSAVQVKNVYENIKGTSATKVAIKFDCS	400
Db	354	IKFQNVEMHNVENPIIIDQNYCDQDKPCQEQSSAVQVKNVYQNIKGTCSNVAITFDCS	413
Qy	401	TNFPCEGIIMENINLVSGSKPSEATCKNVHFNNAEHVTPHCTSLSEISE	451
Db	414	KRFPQGVLEVDVLEIEGGAALKCNVELSETGVVSPHCQEGGEE	464

PGLR_ACTCH	STANDARD;	PRT;	467 AA.
ID AC	P35336;		
DT	01-JUN-1994 (Rel. 29, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DB	Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase).		
OS	Actinidia chinensis (Kiwi) (Yangtao).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;		
OC	Ericales; Actinidiaceae; Actinidia.		
NCBI_TaxID=3625;			
LN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Deliciosa;		
RC	MEDLINE=94302157; PubMed=8029342; DOI=10.1104/pp.103.2.669;		
RA	ACKLINSON R.G., Gardner R.C.;		
RT	"A polygalacturonase gene from kiwifruit (<i>Actinidia deliciosa</i>).";		
RL	Plant Physiol. 103:669-670(1993).		
CC	-1- FUNCTION: Acts in concert with the pectinesterase, in the ripening process. Is involved in cell wall metabolism, specifically in polyuronide degradation.		
CC	-1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-galactosiduronic linkages in pectate and other galacturonans.		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- DEVELOPMENTAL STAGE: In ripening fruit.		
CC	-1- SIMILARITY: Belongs to the glycosyl hydrolase 28 family.		
CC	-----		
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CC	-----		
DR	EMBL; L12019; AAC14453.1; -		
DR	InterPro; IPR000743; Glyco_hydro_28.		
DR	InterPro; IPR006626; Pbh1.		
DR	InterPro; IPR011050; Pectin_lyas_like.		
DR	Pfam; PF00295; Glyco_hydro_28; 1.		
DR	SMART; SM00710; Pbh1; 4.		
DR	PROSITE; PS00502; POLYGALACTURONASE; 1.		
KW	Cell wall; Fruit ripening; Glycoprotein; Glycosidase; Hydrolase;		
KW	Signal.		
FT	SIGNAL	1	27 Potential.
FT	CHAIN	28	467 Polygalacturonase.
FT	ACT_SITE	306	306 Probable.
FT	CARBOHYD	290	290 N-linked (GlcNAc...) (Potential).
SQ	SEQUENCE	467 AA;	50776 MW; 5A9A61483C028B7A CRC64;
Query Match		54.2%;	Score 1295.5; DB 1; Length 467;
Best Local Similarity		54.6%;	Pred. No. 2e-82;
Matches	257;	Conservative	75; Mismatches 112; Indels 27; Gaps 7;
QY	1	MVIQRN--SILLIIIFASSISICTRSNVIDNMLPKQVYDNLIOEFAHDFOAYLSYLSKN	58
Db	1	MAQRFFQFVIITLLIPLSFI LGYTSVHED----PPHYHLE-EGYDFKAYPSYITI	55
QY	59	TESNNINDKVKNGI-----KVINLSFGAKGDKGYTDYINAEQAWNE	101
Db	56	GDNDPGSSMSHENGIFGLRKVDYGMDRVLDASKTNVDDFGAKGDGRD-DTKAFKAWKA	114
QY	102	ACSSRTFPQVVPVKKNNKLLKQITFSGPCRSSISVKIFGSLSEASKISDY-KDRRLWTF	160
Db	115	ACSSSTSSAVLVLPK-KNYLVRPISFGSGGLTQIYGTIEASDDRSYDKRGHRLVLF	173
QY	161	DSVQNLVVGGGGTINGNGOVWPPSSCKINKSLPCRDAPTALTFWNCKNLKYNLKSNAQ	220
Db	174	DSVQNLVVEGGGTINGNGKIWNQNSCKTNKALPKCDAPTALTFFYKSHVIVNLIKENAQ	233
QY	221	QIHKFBSECTNVVASNLMINASAKSPNTDGVHVSNTQYQISDTIIGTGDDCISVSGSQ	280